3D Registration of Human Face Using Evolutionary Computation and Kriging Interpolation

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Abstract: This paper proposes a fast and robust 3D human face geometric data registration strategy dedicated for image-guided medical applications. The registration scheme is composed of a coarse transformation stage and a fine-tuning stage. In the first stage, fuzzy c-mean is used to reduce the data amount of template 3D image, and evolutionary computation is implemented to find optimal initial pose for the Iterative Closest Point plus k-dimensional (K-D) tree scheme. In the second stage, the huge reference image data are replaced by a Kriging model. The time-consuming search for corresponding points in evaluating the degree of misalignment is substituted by projecting the points in the template image onto the model. To illustrate the validity and applicability of the proposed approach, a problem composed of 174,635 points reference image and an 11,280 points template image is demonstrated. Computational results show that our approach accelerates the registration process from 1361.28 seconds to 432.85 seconds when compared with the conventional ICP plus K-D tree scheme, while the average misalignment reduces from 11.35 mm to 2.33 mm.

Keywords: Human face registration; Evolutionary computation; Kriging model; Iterative closest point; Image-guided therapy.

I. INTRODUCTION

Registration of 3D geometric data coming from multimodal images is essential for exploiting the complementary information between them [1-2]. In medical imaging, the data can be obtained from computer tomography (CT), laser range finder, or magnetic resonance imaging (MRI), and the information can be used in image-guided procedures, such as positioning for frameless neurosurgery.

The Iterative Closest Point algorithm (ICP) [3-7], together with the K-D search method (K-D tree) [8], has become a popular registration scheme. Approximate K-D tree search algorithm (AK-D tree) [9] was proposed by excluding the backtracking in K-D tree, which improves runtime efficiency with the sacrifice of reducing the correspondence accuracy. However, these conventional schemes are extremely sensitive to initial trial pose and requires multiple trials to find a reliable solution [1-2]. Besides, the scheme demands huge computing power when large data set is involved in either reference image or template image, which is not uncommon in medical applications. We thus propose a scheme that is both consistent in each run and fast enough to extend the applicability of 3D registration in

To illustrate the validity and applicability of the proposed approach, a problem composed of 174,635 points computer tomography (CT) reference image and a 11,280 points template image, derived from a laser range finder, is provided.

II. THE PROPOSED METHOD

The proposed registration scheme is composed of a coarse transformation stage and a fine-tuning stage.

1. The coarse transformation stage

In the first stage, fuzzy c-mean (FCM) [10] is used to reduce the data amount of template 3D image, and evolutionary computation is implemented to find the global optimal initial pose for the ICP plus K-D tree scheme. The cluster centers in the FCM algorithm are representatives of the large 3D coordinate data, which are used since the data obtained from the laser range finder are generally not evenly distributed [11].

The proposed evolutionary computation method is the so-called island genetic algorithm [12]. The algorithm is based on the biological observation that several subpopulations that occasionally exchanges individuals can be more search-effective than an inclusive one in which all the members are held together.
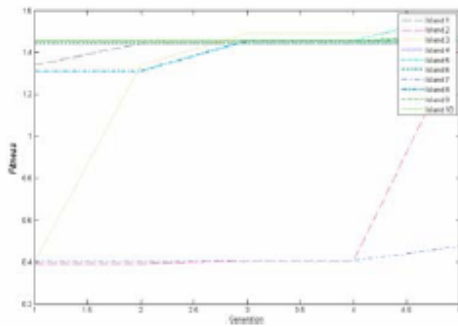
Fig.1. Evolutionary history of a typical parallel genetic
algorithm scheme in 10 islands

Fig. 1 shows a typical evolutionary history of the fitness scores in 10 computing islands. In the optimization problem, a candidate solution, the chromosome, is defined as a set of parameter matrices, i.e., translational component

$$R = \begin{bmatrix} r_{11} & r_{12} & r_{13} \\ r_{21} & r_{22} & r_{23} \\ r_{31} & r_{32} & r_{33} \end{bmatrix},$$

and rotation sub-matrix

$$T = \begin{bmatrix} t_1 \\ t_2 \\ t_3 \end{bmatrix},$$

to be optimized:

$$\vartheta = [r_{11}, r_{12}, r_{13}, r_{21}, r_{22}, r_{23}, r_{31}, r_{32}, r_{33}, t_1, t_2, t_3],$$

where ϑ is usually in expanded cascade form of the parameters R, T. The goal is to minimize the Err. To comply with the maximization formulation in evolutionary computation, each chromosome has a fitness value defined by the approximate inverse of the summation of errors between the corresponding points. The optimization problem is then defined as searching for ϑ to maximize the fitness value. Note that, to comply with the maximization formulation in evolutionary computation, each chromosome has a fitness value defined by the inverse of the misalignment degree.

2. The fine-tuning stage

In the second stage, the huge reference image data are replaced by a Kriging model [13]. Hence, the time-consuming search for corresponding points in evaluation the degree of misalignment is substituted by projecting the points in the template image onto the model. As the transformation has been approximated in the first stage, only slight modification

by the downhill simplex method [14] is required.

In the Kriging model, the relation between the coordinates $\{x, y, z\}$ is represented by

$$z = \beta_1 + x \cdot \beta_2 + y \cdot \beta_3 + x^2 \cdot \beta_4 + x \cdot y \cdot \beta_5 + y^2 \cdot \beta_6 + \sum_{j=1}^{2} e^{-\theta_j \cdot d_j^2} \cdot \gamma^*$$

where correlation factors $\gamma^* \in \Re^n$ and correlation function parameters $\theta = [\theta_1, \theta_2] \in \Re^2$ are solved by the maximum likelihood estimate (MLE) and $\beta = [\beta_1, \beta_2, ..., \beta_6]^T \in \Re^6$ are solved by the least squares estimate (LSE).

To clarify the procedure, we summarize the steps as follows:

Step 1. Calculate the fuzzy c-mean vectors of both the reference image data and the template image data. The clustering centers are used to represent these two huge data sets.

Step 2. Establish the K-D tree of the reduced template image data.

Step 3. Use the parallel genetic algorithms to find the best initial pose of the reference image data for the ICP registration scheme.

Step 4. Build the Kriging model of the (complete) template image data.

Step 5. Use the downhill simplex method to find the best alignment between the reference image data and the Kringing model.

The result of Step 5 is then the final result of the coordinate transformation required for the 3D alignment.

III. NUMERICAL STUDIES

To illustrate the validity and applicability of the proposed approach, a problem composed of 174,635 points computer tomography (CT) reference image and a 11,280 points template image, derived from a laser range finder, is provided.

The alignment between the template data and the Kriging model is shown in Fig. 2 and Fig. 3. Fig. 4 shows a view of successful registration between two 3D images using the proposed scheme, and Fig. 5 is a typical registration result obtained using the conventional ICP plus K-D tree scheme. The possibility of misalignment is more than 12 % since the conventional scheme highly depends on initial pose of the reference image.

The example demonstrated that our approach accelerates the process from 1361.28 seconds to 432.85 seconds (373.46 seconds for the first stage and 59.39 seconds for the second stage) when compared with the conventional ICP plus K-D tree scheme, while the average misalignment reduces from 11.35 mm to 2.33 mm. In the example, 100 runs were conducted for both

635

schemes, our scheme succeeded in each run with equal results. On the contrary, the results of the conventional ICP plus K-D tree scheme vary dramatically.
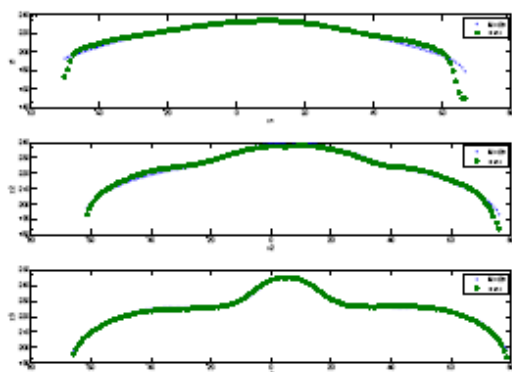

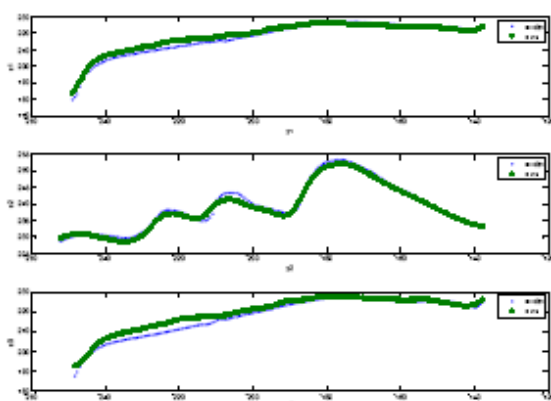Fig. 2. Alignment between the template data and the Kriging model (transverse view)

Fig. 3. Alignment between the template data and the Kriging model (sagittal view)
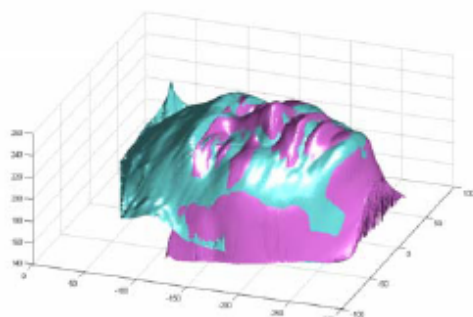

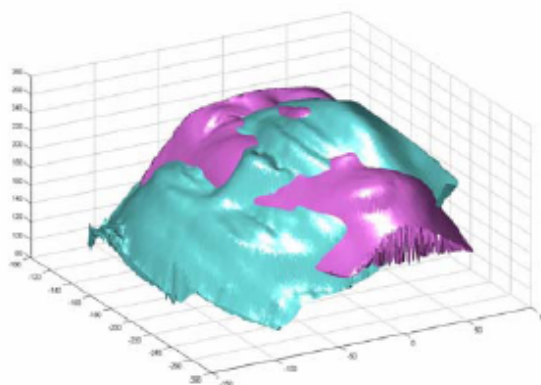Fig. 4. Successful registration of two 3D images using the proposed scheme

Fig. 5. A typical (failed) registration result obtained using the conventional ICP plus K-D tree scheme

VI. CONCLUSION

Registration of 3D geometric data is essential in exploiting the complementary information between them. The Iterative Closest Point algorithm, together with the K-D search method, has become a popular registration scheme. However, the conventional scheme is extremely sensitive to initial pose and demands huge computing power when large data set is involved.

In this paper, we propose a fast and accurate 3D registration scheme for human face data. The scheme combines evolutionary computation, the Kriging surrogate model, and the down-hill simplex method.

We conduct the experiment between a 174,635 points computer tomography (CT) reference image and an 11,280 points template image obtained from a laser range finder. The result shows that our approach outperforms the conventional ICP plus K-D tree scheme with execution time reduced from 1361.28 seconds to 432.85 seconds, and the average misalignment reduced from 11.35 mm to 2.33 mm.

Potential applications of the proposed 3D alignment methodology include accurate positioning for medical surgery and pose invariant face recognition.

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